Three divergent subpopulations of the malaria *Parasite plasmodium* knowlesi

ABSTRACT

Multilocus microsatellite genotyping of Plasmodium knowlesi isolates previously indicated 2 divergent parasite subpopulations in humans on the island of Borneo, each associated with a different macaque reservoir host species. Geographic divergence was also apparent, and independent sequence data have indicated particularly deep divergence between parasites from mainland Southeast Asia and Borneo. To resolve the overall population structure, multilocus microsatellite genotyping was conducted on a new sample of 182 P. knowlesi infections (obtained from 134 humans and 48 wild macaques) from diverse areas of Malaysia, first analyzed separately and then in combination with previous data. All analyses confirmed 2 divergent clusters of human cases in Malaysian Borneo, associated with long-tailed macaques and pig-tailed macaques, and a third cluster in humans and most macaques in peninsular Malaysia. High levels of pairwise divergence between each of these sympatric and allopatric subpopulations have implications for the epidemiology and control of this zoonotic species.

Keyword: Plasmodium knowlesi; Zoonotic malaria parasite; Infectious Diseases